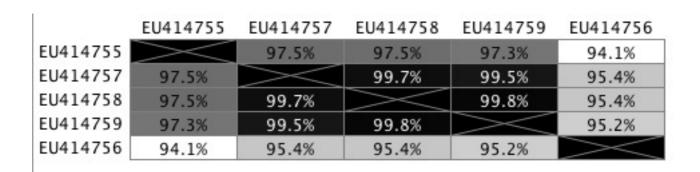
## A) No. differences incl. gaps in ITS1 region

	EU414755	EU414757	EU414758	EU414759	EU414756
EU414755		14	15	15	27
EU414757	14		1	1	20
EU414758	15	1	7	0	19
EU414759	15	1	0		19
EU414756	27	20	19	19	

## B) Percentage identity in ITS1 region

	EU414755	EU414757	EU414758	EU414759	EU414756
EU414755		93.2%	92.8%	92.8%	87.1%
EU414757	93.2%		99.5%	99.5%	90.2%
EU414758	92.8%	99.5%		100%	90.6%
EU414759	92.8%	99.5%	100%		90.6%
EU414756	87.1%	90.2%	90.6%	90.6%	

## C) Percentage identity over whole sequence 171bp 18S, 198-207bp ITS1, 159bp 5.8S and 51-52bp ITS2



**SuppFig. 3.** Intragenomic variation in ITS sequences among the five clones sequenced from isolate GE09. 18S boundary ends with GATCATTA and 5.8S begins with CAACTTT, according to the convention of Hibbett et al. (1995).